



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/070,489
Source: PCT 10
Date Processed by STIC: 3/21/02

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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Does Not Comply
Corrected Diskette Needed

PCT10

Errors on pp. 3, 6-10,

13-14

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/070,489

DATE: 03/21/2002

TIME: 14:52:18

Input Set : A:\1104seq.us1

Output Set: N:\CRF3\03212002\J070489.raw

3 <110> APPLICANT: Glare, Travis T
 4 Hurst, Mark R H
 5 Jackson, Trevor A
 7 <120> TITLE OF INVENTION: Insecticidal nucleotide sequences
 9 <130> FILE REFERENCE: sepA sepB sepC ORF1 and ORF2
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/070,489
 12 <141> CURRENT FILING DATE: 2001-03-01
 14 <150> PRIOR APPLICATION NUMBER: PCT/NZ00/00174
 15 <151> PRIOR FILING DATE: 2000-09-04
 17 <150> PRIOR APPLICATION NUMBER: NZ 337610
 18 <151> PRIOR FILING DATE: 1999-09-02
 20 <160> NUMBER OF SEQ ID NOS: 6
 22 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

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 26 <212> TYPE: DNA
 27 <213> ORGANISM: Serratia entomophila
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 40 <221> NAME/KEY: CDS
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 42 <223> OTHER INFORMATION: SepC
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 47 <223> OTHER INFORMATION: ORF1
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 50 <221> NAME/KEY: CDS
 51 <222> LOCATION: (13908)..(14483)
 52 <223> OTHER INFORMATION: ORF2
 54 <220> FEATURE:
 55 <221> NAME/KEY: misc_feature

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56 <222> LOCATION: (1955)..(18937)
57 <223> OTHER INFORMATION: MINIMUM SEQUENCE REQUIRED FOR PATHOGENICITY AS
58   DEFINED BY DELETION AND TRANSPOSON MUTAGENESIS
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63 caacgtggca atggatgttg tttgtgtcgg tatgaatcgc cgcaacgtac tgggtgttctg 120
65 acataccagc tgccgataaa ctgtgacgaa cactatcaaa gatgtgttcc gtcgacctga 180
67 aagccaggat ttattttttac accaatgggtt ggggtgggctt cctttctgaa ctgggtgcac 240
69 atttagccgg catcatcaaa agatgcatgg aaatacaaat atcatattta cagacacca 300
71 agttgatgac ctgctccgtg agttgaaatg ccgacggggg aaatcagcag ccttttcaac 360
73 tcatggagca gggggaaaac aatcctcaat aaccgcgatt ggatatactg ccagtgtgca 420
75 ttttaacctt ttagtgtgtt tccttaatat cccaatcggt gaatcgctac atacggcaga 480
77 cattagtatc tcacttatca tcaaagtaat atcacaccga gaatgctaatt ttcattgat 540
79 gaaaacgttc cattaataaa ttttcagaaa cctaacacgg catttttatg ctgatcagt 600
81 aattgattgt ttctgaaaaa attaattgca cctctgccac ttatcagata aaaacacccc 660
83 atgcggtaag ttttttattt tttattaatg attttattaa tgattttatt aatgatttta 720
85 ttaatgattt tattaatgat tttactatag atgaatgtta acatgggtga taatttactt 780
87 tactcaattt aattgttggg atgaccatgt tttagatgag tggcacggat tcattattgt 840
89 aaaaaaagta tctaaaacct ttagcagcaa tcctacttga ggatgacctc gacaggactt 900
91 gattattgcc attttttacg aaggaagatg acgggtgata aataataaaa aaaacaaaag 960
93 tatagcetta ggtatcgccg attacatcca gtaacactta ttgacttttt tttacttcta 1020
95 ccgttagcta taaatatgat atttaaactc gtatttttat ataaaaccag tttatgatgc 1080
97 tggattgggc attaaagtcg ttatatgtga tcgttatctg tcattgattg gtgtttaatc 1140
99 ttttattctt ccagtggagt ttcaggggga atgtattggg taatcatact catgtcattt 1200
101 gttgctttga tgtaaatta acgtgttcat tcattatggt ctactgttgt ttctattgtc 1260
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111 tgggtgcctt gttaccagcg ccgtgacggg gaagcttttt gttatcatta tgagcaagat 1560
113 agagagaaaa tatcttgagg aataaccgcc atgttccaaa tcatacttct taatgttaat 1620
115 gccgtgattt gcttggtctat tgccgtcaga ttattcctgt ggcgtatcaa tcataaaatg 1680
117 aaaaacattg tcgtctcttt tattgctttt ctcatattta cggcgtgagg cgctgtctcc 1740
119 atcaggacga tgacggggga gtattactat gcgattggg cggagacgat cattaacctt 1800
121 tcgcttttcc tgtctgttta tatacgcaat ggcgaaatcc ttcggtgggg ggagaaaaa 1859
123 atg aag ata agt tcc cga ggt atc gca tta atc aaa gag ttc gaa ggt 1907
124 Met Lys Ile Ser Ser Arg Gly Ile Ala Leu Ile Lys Glu Phe Glu Gly
125 1 5 10 15
127 ctg cgc tta cac gct tat cgc tgc gcc gct gac gtc tgg act gtc ggt 1955
128 Leu Arg Leu His Ala Tyr Arg Cys Ala Ala Asp Val Trp Thr Val Gly
129 20 25 30
131 tat ggc cac acg gca ggg gtt aca aag ggt gac atc atc acg gtc gat 2003
132 Tyr Gly His Thr Ala Gly Val Thr Lys Gly Asp Ile Ile Thr Val Asp
133 35 40 45
135 gaa gcc cag acg atg ctg aca aac gat att acc gta ttt gaa cgg gcg 2051
136 Glu Ala Gln Thr Met Leu Thr Asn Asp Ile Thr Val Phe Glu Arg Ala
137 50 55 60
139 gtc agt cag gcc gtc gcg gtt cct ctg aat cag tcg caa tac gat gcc 2099
140 Val Ser Gln Ala Val Ala Val Pro Leu Asn Gln Ser Gln Tyr Asp Ala

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141 65          70          75          80
143 ctg gtt tct ttg gtt ttt aat att ggc cag ggg aat ttt aaa cgc tct 2147
144 Leu Val Ser Leu Val Phe Asn Ile Gly Gln Gly Asn Phe Lys Arg Ser
145          85          90          95
147 acc ttg ttg aaa aaa ctc aac aaa cag gac tat gtc ggc gcc ggg aac 2195
148 Thr Leu Leu Lys Lys Leu Asn Lys Gln Asp Tyr Val Gly Ala Gly Asn
149          100          105          110
151 gag ttt tta cgc tgg acc cgg gcc aat ggg aag gtc ctt ccc gga ctg 2243
152 Glu Phe Leu Arg Trp Thr Arg Ala Asn Gly Lys Val Leu Pro Gly Leu
153          115          120          125
155 att cgc cga cgc gaa gct gaa cgg gtg ttg ttt gag aaa ctg ggt gca 2291
156 Ile Arg Arg Arg Glu Ala Glu Arg Val Leu Phe Glu Lys Leu Gly Ala
157          130          135          140
159 taa ccctttgcga cgtaccacaca agatgaagat aacaccgcgt actgagcgg 2344
E--> 161 (145) → delete, do not place an amino acid number under a stop codon; please
163 ggcgcaacaa tgaataaatg actgtgtacg gcctgtcctt cacaacggat gggaccatca 2404
165 acgtaa tga atg agg caa gac att atg tat aat att gat gat att ctg 2452
166 Met Arg Gln Asp Ile Met Tyr Asn Ile Asp Asp Ile Leu
W--> 167          150          155
169 gag aaa gtg aat gct cca cga gca cgc ctg tca gaa gaa aac gat aca 2500
170 Glu Lys Val Asn Ala Pro Arg Ala Arg Leu Ser Glu Glu Asn Asp Thr
W--> 171 160          165          170          175
173 gcg gtg acg ctg acg gat tta ttc tcg cgt tcg ttt ccc gag gtc aaa 2548
174 Ala Val Thr Leu Thr Asp Leu Phe Ser Arg Ser Phe Pro Glu Val Lys
W--> 175          180          185          190
177 aaa atc act ggc gac agc ctg tca tgg gga gag gtc tgc tat ctg tac 2596
178 Lys Ile Thr Gly Asp Ser Leu Ser Trp Gly Glu Val Cys Tyr Leu Tyr
W--> 179          195          200          205
181 agt cag gcg cag cac gaa cag aaa gaa aac cgg ctc acc gaa tcc cgt 2644
182 Ser Gln Ala Gln His Glu Gln Lys Glu Asn Arg Leu Thr Glu Ser Arg
W--> 183          210          215          220
185 att ctg gcc cgg gcg aat ccc cta ctg gtg aat gcc gtt cgc ctg gga 2692
186 Ile Leu Ala Arg Ala Asn Pro Leu Leu Val Asn Ala Val Arg Leu Gly
W--> 187          225          230          235
189 ata cgg cag gca gcc ggc agt cgc agc tat gat gac tgg ttt ggc tcc 2740
190 Ile Arg Gln Ala Ala Gly Ser Arg Ser Tyr Asp Asp Trp Phe Gly Ser
W--> 191 240          245          250          255
193 cgc gca gac cgt ttc gcc cgc ccc gcc tcg gtg gcc tcc atg ttc tca 2788
194 Arg Ala Asp Arg Phe Ala Arg Pro Gly Ser Val Ala Ser Met Phe Ser
W--> 195          260          265          270
197 ccg gcg gcg tat ctg acc gag ctg tac cgt gag gcg aag gac ctg cat 2836
198 Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asp Leu His
W--> 199          275          280          285
201 ccg gac acc tcg ctg ttc cgg ctg gac atc cgg cgt ccc gac ctg gcg 2884
202 Pro Asp Thr Ser Leu Phe Arg Leu Asp Ile Arg Arg Pro Asp Leu Ala
W--> 203          290          295          300
205 gcg ctg gcc ctt agc cag aat aat atg gac gac gag ctc tcc acc ctg 2932
206 Ala Leu Ala Leu Ser Gln Asn Met Asp Asp Glu Leu Ser Thr Leu
W--> 207          305          310          315

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adjust
Subsequent
numbering

* Due to size of sequence, only this page shown as a sample of numbering adjustments to be made.

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1465 accgccgcgcg gtaacggaga cgtggatatg cggatgttga ttgagctgcc ggccttaggt 18877
 1467 gtggagcgcg caaaaaatgc cggcctcgat gccctgccgg cgtgcccgagc ggagcatggc 18937
 1560 <210> SEQ ID NO: 4
 1561 <211> LENGTH: 2376
 1562 <212> TYPE: PRT
 1563 <213> ORGANISM: Serratia entomophila
 1565 <220> FEATURE:
 1566 <223> OTHER INFORMATION: SepA amino acid sequence encoding an insecticidal protein

when

1567 linked with at least SEQ ID NO: 1
 1569 <400> SEQUENCE: 4
 1570 Met Arg Gln Asp Ile Met Tyr Asn Ile Asp Asp Ile Leu Glu Lys Val
 1571 1 5 10 15
 1573 Asn Ala Pro Arg Ala Arg Leu Ser Glu Glu Asn Asp Thr Ala Val Thr
 1574 20 25 30
 1576 Leu Thr Asp Leu Phe Ser Arg Ser Phe Pro Glu Val Lys Lys Ile Thr
 1577 35 40 45
 1579 Gly Asp Ser Leu Ser Trp Gly Glu Val Cys Tyr Leu Tyr Ser Gln Ala
 1580 50 55 60
 1582 Gln His Glu Gln Lys Glu Asn Arg Leu Thr Glu Ser Arg Ile Leu Ala
 1583 65 70 75 80
 1585 Arg Ala Asn Pro Leu Leu Val Asn Ala Val Arg Leu Gly Ile Arg Gln
 1586 85 90 95
 1588 Ala Ala Gly Ser Arg Ser Tyr Asp Asp Trp Phe Gly Ser Arg Ala Asp
 1589 100 105 110
 1591 Arg Phe Ala Arg Pro Gly Ser Val Ala Ser Met Phe Ser Pro Ala Ala
 1592 115 120 125
 1594 Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asp Leu His Pro Asp Thr
 1595 130 135 140
 1597 Ser Leu Phe Arg Leu Asp Ile Arg Arg Pro Asp Leu Ala Ala Leu Ala
 1598 145 150 155 160
 1600 Leu Ser Gln Asn Asn Met Asp Asp Glu Leu Ser Thr Leu Ser Leu Ser
 1601 165 170 175
 1603 Asn Glu Leu Leu Tyr Arg Gly Ile Gly Ala Ala Glu Gly Leu Asp Asp
 1604 180 185 190
 1606 Asp Ser Val Arg Glu Leu Leu Ala Gly Tyr Arg Leu Thr Gly Leu Thr
 1607 195 200 205
 1609 Pro Tyr His Trp Ala Tyr Glu Ala Ala Arg Gln Ala Ile Leu Val Gln
 1610 210 215 220
 1612 Asp Pro Thr Leu Met Gly Phe Ser Arg Asn Pro Asp Val Ala Gln Leu
 1613 225 230 235 240
 1615 Met Asp Pro Ala Ser Met Leu Ala Ile Glu Ala Asp Ile Ser Pro Glu
 1616 245 250 255
 1618 Leu Tyr Gln Ile Leu Ala Glu Glu Ile Thr Thr Asp Ser Tyr Glu Ala
 1619 260 265 270
 1621 Leu Trp Ser Lys Asn Phe Gly Asp Met Pro Pro Ser Ser Leu Leu Ser
 1622 275 280 285
 1624 Tyr Asp Ala Leu Ala Thr Phe Tyr Asp Leu Asp Tyr Asp Glu Leu Thr
 1625 290 295 300
 1627 Ser Leu Leu Ser Leu Arg Leu Asp Phe Ser Asn Pro Asn Asn Glu Tyr

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Input Set : A:\1104seq.us1

Output Set: N:\CRF3\03212002\J070489.raw

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1628 305          310          315          320
1630 Tyr Ile Asn Ser Gln Leu Ser Val Val Thr Leu Asn Glu Ser Thr Gly
1631          325          330          335
1633 Leu Ile Thr Ile His His Tyr Leu Arg Thr Leu Gly Gly Asp Ser Gln
1634          340          345          350
1636 Gln Ile Asn Pro Glu Leu Ile Pro Tyr Gly Asp Gly Thr Tyr Leu Tyr
1637          355          360          365
1639 Asn Phe Ser Val Val Ser Thr Ile Ser Glu Asp Ser Phe Lys Leu Gly
1640          370          375          380
1642 Ser Leu Gly Ser Asn Ser Ser Asn Leu Tyr Ser Gly Asp Tyr Gln Leu
1643 385          390          395          400
1645 Gln Lys Gly Val Arg Tyr Ser Ile Pro Val Glu Ile Asp Glu Gly Lys
1646          405          410          415
1648 Leu Asn Asp Gly Ile Thr Ile Gly Leu Ser Arg Lys Gly Gly Tyr
1649          420          425          430
1651 Tyr Ser Thr Val Asn Phe Thr Leu Ile Glu Tyr Asp Pro Ala Ile Phe
1652          435          440          445
1654 Ile Leu Lys Leu Asn Lys Val Ile Arg Leu Tyr Lys Ala Thr Gly Met
1655          450          455          460
1657 Thr Thr Ala Glu Ile Tyr Gln Ile Thr Asn Ile Leu Asn Asn Gly Leu
1658 465          470          475          480
1660 Thr Ile Asp His Ala Val Leu Ser Lys Ile Phe Leu Val Arg Tyr Leu
1661          485          490          495
1663 Met Arg His Tyr Gln Leu Asp Val Ala Arg Ser Leu Ile Leu Cys Asn
1664          500          505          510
1666 Gly Thr Ile Ser Asp Gln Ala Phe Ser Gly Glu Thr Gly Leu Phe Thr
1667          515          520          525
1669 Thr Leu Phe Asn Thr Pro Pro Leu Asn Gly Gln Leu Phe Ser Ala Asp
1670          530          535          540
1672 Asp Thr Pro Leu Asp Leu Arg Ser Glu Ala Pro Glu Asp Ala Phe Arg
1673 545          550          555          560
1675 Leu Ser Val Leu Lys Arg Ala Phe Asn Ile Ser Ala Ser Gly Leu Ser
1676          565          570          575
1678 Thr Leu Trp Gln Leu Ala Ser Gly Asp Ser Ser Ala Gly Phe Ser Cys
1679          580          585          590
1681 Ser Ala Asp Asn Ile Ala Ala Leu Tyr Arg Val Lys Leu Leu Ala Asp
1682          595          600          605
1684 Ile His Asp Leu Ser Ala Gly Glu Leu Ser Met Leu Leu Ser Val Ser
1685          610          615          620
1687 Pro Phe Ser Gly Val Ala Ala Gly Ser Leu Ser Asp Asn Glu Leu Thr
1688 625          630          635          640
1690 Gln Phe Leu Tyr Gln Thr Thr Thr Trp Leu Thr Glu Gln Gly Trp Thr
1691          645          650          655
1693 Val Ser Asp Val Phe Leu Met Leu Thr Thr Gln Tyr Gly Thr Leu Leu
1694          660          665          670
1696 Thr Pro Asp Ile Glu Asn Leu Leu Ala Ser Leu Arg Asn Gly Leu Ser
1697          675          680          685
1699 Gly Arg Glu Leu Phe Pro Glu Thr Leu Pro Gly Asp Gly Ala Pro Phe
1700          690          695          700

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1708 Phe Ile Leu Leu Val Met Asn Ala Ala Pro Asn Asp Glu Gln Ala Gly
1709 740 745 750
1711 Gln Met Ala Gly Phe Cys Gln Ala Leu Trp Gln Leu Ala Leu Ile Ile
1712 755 760 765
1714 Arg Ser Thr Gly Leu Ser Thr Arg Glu Leu Thr Leu Leu Val Ser Gln
1715 770 775 780
1717 Pro Gly Arg Phe Arg Thr Gly Trp His His Leu Pro His Asp Leu Pro
1718 785 790 795 800
1720 Ala Leu Arg Asp Ile Thr Arg Phe His Ala Val Val Asn Arg Ser Gly
1721 805 810 815
1723 Ser His Ala Gly Glu Val Leu Thr Ala Leu Glu Thr Gly Glu Leu Ser
1724 820 825 830
1726 Ser Ala Leu Leu Ala Arg Ala Leu Ser Gln Asn Glu Gln Asp Val Thr
1727 835 840 845
1729 Gly Ala Leu Ala Gln Val Arg Gly Ala Gly Glu Gln Asp Asn Ser Val
1730 850 855 860
1732 Phe Thr Ser Trp Glu Glu Val Asp Gln Ala Glu Gln Trp Leu Asp Met
1733 865 870 875 880
1735 Ser Glu Thr Leu Ser Ile Thr Pro Ser Gly Leu Ala Ser Leu Ile Ala
1736 885 890 895
1738 Leu Lys Tyr Ile Asn Val Ser Asp Asp Ser Ala Pro Leu Tyr Ser Gln
1739 900 905 910
1741 Trp Gln Val Val Ser Gly Leu Leu Gln Ala Gly Leu Lys Ser Ser Gln
1742 915 920 925
1744 Ser Ser Ala Leu His Asp Tyr Leu Glu Glu Gly Thr Ser Ser Ala Leu
1745 930 935 940
1747 Cys Ala Tyr Tyr Leu Arg Asn Leu Ala Pro Asn Met Val Ser Gly Arg
1748 945 950 955 960
1750 Asp Asp Leu Phe Gly Tyr Leu Leu Leu Asp Asn Gln Val Ser Ala Lys
1751 965 970 975
1753 Val Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Gly Ile Arg Leu Tyr
1754 980 985 990
1756 Ile Asn Arg Ala Leu Asn Gly Ile Glu Leu Ser Ala Met Ala Glu Val
1757 995 1000 1005
1759 Arg Gly Arg Gln Phe Phe Thr Asp Trp Asp Thr Phe Asn Lys Arg Tyr
1760 1010 1015 1020
1762 Ser Thr Trp Ala Gly Val Ser Glu Leu Val Tyr Tyr Pro Glu Asn Tyr
E--> 1763 025 1030 1035 1040
1765 Leu Asp Pro Thr Val Arg Ile Gly Gln Thr Gly Met Met Asp Thr Leu
1766 1045 1050 1055
1768 Leu Gln Ser Val Ser Gln Ser Ser Ile Asn Arg Asp Thr Val Glu Asp
1769 1060 1065 1070
1771 Ala Phe Lys Thr Tyr Leu Thr Thr Phe Glu Gln Ile Ala Asn Leu Asn
1772 1075 1080 1085
1774 Thr Val Ser Gly Tyr His Asp Asn Ala Ser Met Thr Gln Gly Thr Thr

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→ Please align the first digit (1 in 1025) immediately underneath the first letter of the first amino acid appearing in a line. Some error repeated throughout this sequence and the next sequence.

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1780 Ser Ala Asn His Ser Lys Ile Gln Asp Ser Met Met Pro Ala Asn Ala
1781      1125      1130      1135
1783 Trp Thr Gly Trp Thr Lys Ile Asn Cys Gly Met Asn Pro Trp Ser Asp
1784      1140      1145      1150
1786 Leu Val Cys Ser Val Phe Phe Asn Ser Arg Leu Tyr Val Val Trp Val
1787      1155      1160      1165
1789 Glu Glu Asn Gln Ser Ala Asp Thr Glu Ala Glu Ser Thr Thr Thr Thr
1790      1170      1175      1180
1792 Gln Gln Ser Tyr Thr Leu Lys Leu Ser Phe Arg Arg Tyr Asp Gly Thr
E--> 1793 185      1190      1195      1200
1795 Trp Ser Ser Pro Val Ser Phe Asp Ile Thr Gly Asn Ile Ala Phe Pro
1796      1205      1210      1215
1798 Glu Thr Gln Gly Met His Val Thr Cys Asn Pro Leu Thr Glu Gln Leu
1799      1220      1225      1230
1801 Tyr Cys Ala Phe Tyr Ser Val Thr Ser Lys Pro Asp Phe Asp Asn Ala
1802      1235      1240      1245
1804 Gln Leu Ile Ser Val Asp Asn Asp Met Thr Leu Asn Val Ile Ser Asp
1805      1250      1255      1260
1807 Ile Gly Ile Phe Lys Ser Val Ser His Glu Phe Asn Thr Ser Thr Glu
E--> 1808 265      1270      1275      1280
1810 Lys Phe Ile Asn Asn Val Phe Ser Asp Pro Ser Ala Asn Tyr Phe Val
1811      1285      1290      1295
1813 Ser Ala Thr Ser Leu Ile Asp Asp Val Ile His Ser Asp Phe Ser Leu
1814      1300      1305      1310
1816 Leu Asn Ser Lys Thr Thr Ser Thr Val Phe Thr Asn Glu Asp Ser Ser
1817      1315      1320      1325
1819 Leu Leu Thr Pro Glu Leu His Ile Thr Ala Asn Val Ser Cys Phe Val
1820      1330      1335      1340
1822 Ser Thr Ala Gly Ile Ala Thr Gln Ser Thr Ile Glu Lys Phe Val Gln
E--> 1823 345      1350      1355      1360
1825 Ala Gly Ile Glu Phe Glu Glu Ile Asn Phe Tyr Ala Gly Gln Ala Ala
1826      1365      1370      1375
1828 Gly Gly Phe Asp Gly Phe Val Gly Val Asp Val Ser Asn Ser Lys Val
1829      1380      1385      1390
1831 Tyr Gln Val Gly Lys Glu Ala Val Gly Val Thr Val Lys Ser Tyr Ser
1832      1395      1400      1405
1834 Val Thr Gly Val Ser Gly Ser Val Glu Leu Phe Ile Asp Ser Ser Asn
1835      1410      1415      1420
1837 Lys Tyr Phe Ser Gly Ile Leu Ser Asp Lys Met Ile Thr Ala Leu Ile
E--> 1838 425      1430      1435      1440
1840 Ser Gly Ser Thr Ser Lys Val Asn Tyr Val Ser Ser Ile Gly Ser Gln
1841      1445      1450      1455
1843 Asp Phe Trp Ser Val Lys Ser Leu Met Pro Ala Leu Gln Ile Tyr Glu
1844      1460      1465      1470
1846 Leu Ile Asp Asp Ile Ile Leu Thr Ser Gly Val Asn Gly Thr Glu Ile
1847      1475      1480      1485

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Output Set: N:\CRF3\03212002\J070489.raw

```

1849 Lys Ser Trp Pro Ser Ala Glu Trp Tyr Asn Asp Lys Leu Ser Leu Gln
1850      1490      1495      1500
E--> 1852 Ser Gly Asn Asn Leu Phe Asn Thr Lys Ser Leu Ser Phe Thr Val Asn
      1853 505      1510      1515      1520
1855 Thr Ser Asp Ile Val Glu Asp Glu Phe Asp Val Thr Phe Thr Phe Thr
1856      1525      1530      1535
1858 Ala Val Asp Gln Asn Asn Val Val Leu Ala Ala Arg Thr Ala Ile Leu
1859      1540      1545      1550
1861 Thr Val Ile Arg Asn Ile Asn Asn Asp Thr Ser Val Ile Ala Leu Arg
1862      1555      1560      1565
1864 Lys Asn Thr Arg Gly Ala Gln Tyr Ile Arg Phe Thr Ala Gly Asn Asp
1865      1570      1575      1580
1867 Val Ala Leu Ile Arg Leu Asn Thr Leu Phe Ala Arg Gln Leu Val Asp
E--> 1868 585      1590      1595      1600
1870 Arg Ala Asn Thr Gly Ile Asp Thr Ile Leu Ser Met Glu Thr Gln Arg
1871      1605      1610      1615
1873 Leu Thr Glu Pro Ala Leu Glu Glu Gly Ser Asp Val Phe Met Asp Phe
1874      1620      1625      1630
1876 Ser Gly Ala Asn Ala Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro
1877      1635      1640      1645
1879 Met Met Val Phe Gln Arg Leu Leu Gln Glu Gln His Phe Pro Glu Ala
1880      1650      1655      1660
1882 Thr Arg Trp Leu Gln Tyr Val Trp Asn Pro Ala Gly His Val Val Asn
E--> 1883 665      1670      1675      1680
1885 Gly Val Leu Gln Asn Tyr Thr Trp Asn Val Arg Pro Leu Glu Glu Asp
1886      1685      1690      1695
1888 Thr Gly Trp Asn Asp Ser Pro Leu Asp Ser Ile Asp Pro Asp Ala Ile
1889      1700      1705      1710
1891 Ala Gln Tyr Asp Pro Met His Tyr Lys Val Ala Thr Phe Met Ser Tyr
1892      1715      1720      1725
1894 Leu Asp Leu Leu Ile Ala Arg Gly Asp Ala Ala Tyr Arg Leu Leu Glu
1895      1730      1735      1740
1897 Arg Asp Thr Leu Asn Glu Ala Arg Met Trp Tyr Val Gln Ala Leu Asn
E--> 1898 745      1750      1755      1760
1900 Leu Leu Gly Asp Glu Pro Tyr Ile Ser Phe Asp Ala Asp Trp Ser Ala
1901      1765      1770      1775
1903 Leu Thr Leu Gly Asp Ala Ala Ser Glu Val Thr Arg Arg Asp Tyr Gln
1904      1780      1785      1790
1906 Glu Ala Leu Leu Ala Val Arg Arg Leu Val Pro Ala Pro Glu Thr Arg
1907      1795      1800      1805
1909 Thr Ala Asn Ser Leu Thr Ala Leu Phe Leu Pro Gln Gln Asn Glu Val
1910      1810      1815      1820
1912 Leu Lys Gly Tyr Trp Gln Thr Leu Ala Gln Arg Leu His Asn Leu Arg
E--> 1913 825      1830      1835      1840
1915 His Asn Leu Ser Ile Asp Gly Gln Pro Leu Ser Leu Ser Val Tyr Ala
1916      1845      1850      1855
1918 Thr Pro Ser Glu Pro Ser Ala Leu Gln Ser Ala Val Val Asn Ser Ala
1919      1860      1865      1870
1921 Gln Gly Ala Ala Ala Leu Pro Ala Ala Val Met Pro Leu Tyr Ser Phe

```

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Input Set : A:\1104seq.us1

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```

1922      1875      1880      1885
1924 Pro Val Met Leu Glu Asn Ala Arg Gly Met Val Ser Leu Leu Thr Gly
1925      1890      1895      1900
1927 Phe Gly Asn Thr Leu Leu Gly Ile Thr Glu Arg Gln Asp Ala Glu Ala
E--> 1928 905      1910      1915      1920
1930 Leu Ala Lys Leu Leu Gln Thr Gln Gly Ser Glu Leu Ile Arg Gln Gly
1931      1925      1930      1935
1933 Leu Arg Gln Gln Asp Asn Val Leu Glu Glu Ile Asp Ala Asp Ile Ala
1934      1940      1945      1950
1936 Ala Leu Glu Glu Ser Arg Arg Gly Ala Gln Met Arg Phe Glu Arg Tyr
1937      1955      1960      1965
1939 Lys Val Leu Tyr Glu Ala Asp Val Asn Thr Gly Glu Lys Gln Ala Met
1940      1970      1975      1980
1942 Asp Leu Tyr Leu Ser Ser Ser Val Leu Ser Ala Ser Thr Ala Ala Leu
E--> 1943 985      1990      1995      2000
1945 Phe Leu Ala Glu Ala Ala Ala Asp Met Leu Pro Asn Ile Tyr Gly Leu
1946      2005      2010      2015
1948 Ala Val Gly Gly Ser Arg Tyr Gly Ala Leu Phe Lys Ala Thr Ala Ile
1949      2020      2025      2030
1951 Gly Ile Gln Val Ser Ser Asp Ala Thr Arg Ile Ser Ala Asp Lys Ile
1952      2035      2040      2045
1954 Ser Gln Ser Glu Val Tyr Arg Arg Arg Arg Glu Glu Trp Glu Ile Gln
1955      2050      2055      2060
1957 Arg Asp Ser Ala Gln Ser Asp Val Ala Gln Ile Asp Ala Gln Leu Ala
E--> 1958 065      2070      2075      2080
1960 Ala Met Ala Val Arg Arg Glu Gly Ala Glu Leu Gln Lys Thr Tyr Leu
1961      2085      2090      2095
1963 Glu Thr Gln Gln Thr Gln Ala Gln Ala Gln Leu Ala Phe Leu Gln Ser
1964      2100      2105      2110
1966 Lys Phe Asn Asn Thr Ala Leu Tyr Ser Trp Leu Arg Gly Arg Leu Ser
1967      2115      2120      2125
1969 Ala Ile Tyr Tyr Gln Phe Tyr Asp Leu Ala Val Ser Arg Cys Leu Met
1970      2130      2135      2140
1972 Ala Gln Gln Ala Trp Gln Trp Asp Lys Phe Glu Thr Arg Ser Phe Ile
E--> 1973 145      2150      2155      2160
1975 Gln Pro Gly Ala Trp Met Gly Ala Asn Ala Gly Leu Leu Ala Gly Glu
1976      2165      2170      2175
1978 Thr Leu Met Leu Asn Leu Ala Gln Met Glu Gln Ala Trp Leu Thr Gly
1979      2180      2185      2190
1981 Asp Glu Arg Ala Ile Glu Val Thr Arg Thr Val Cys Leu Ser Glu Val
1982      2195      2200      2205
1984 Tyr Thr Ser Leu Ala Glu Asp Ala Ala Phe Ser Leu Ala Asp Lys Val
1985      2210      2215      2220
1987 Val Glu Leu Val Ser Asn Gly Ser Gly Ser Ala Gly Thr Lys Ser Asn
E--> 1988 225      2230      2235      2240
1990 Gly Leu Gln Met Asp Gln Gln Gln Leu Glu Ala Thr Leu Lys Leu Ala
1991      2245      2250      2255
1993 Asp Leu Gly Ile Gly Asn Asp Tyr Pro Val Ser Leu Gly Thr Met Arg
1994      2260      2265      2270

```

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```

1996 Arg Ile Lys Gln Ile Ser Val Thr Leu Pro Ala Leu Val Gly Pro Tyr
1997      2275      2280      2285
1999 Gln Asp Val Arg Ala Val Leu Ser Tyr Gly Gly Ser Met Val Met Pro
2000      2290      2295      2300
2002 Arg Gly Cys Ser Ala Leu Ala Val Ser His Gly Met Asn Asp Ser Gly
E--> 2003 305      2310      2315      2320
2005 Gln Phe Gln Leu Asp Phe Asn Asp Pro Arg Tyr Leu Pro Phe Glu Gly
2006      2325      2330      2335
2008 Leu Pro Val Asp Asp Thr Gly Thr Leu Thr Leu Ser Phe Pro Asp Ala
2009      2340      2345      2350
2011 Asp Gly Lys Gln Gln Ala Met Leu Leu Ser Leu Ser Asp Ile Ile Leu
2012      2355      2360      2365
2014 His Ile Arg Tyr Thr Ile Ile Ser
2015      2370      2375
2019 <210> SEQ ID NO: 5
2020 <211> LENGTH: 1428
2021 <212> TYPE: PRT
2022 <213> ORGANISM: Serratia entomophila
2024 <220> FEATURE:
2025 <223> OTHER INFORMATION: SepB amino acid sequence encoding an insecticidal protein

```

when

```

2026      linked with at least SEQ ID NO: 1
2028 <400> SEQUENCE: 5
2029 Met Gln Asn His Gln Asp Met Ala Ile Thr Ala Pro Thr Leu Pro Ser
2030 1      5      10      15
2032 Gly Gly Gly Ala Val Thr Gly Leu Lys Gly Asp Ile Ala Ala Ala Gly
2033      20      25      30
2035 Pro Asp Gly Ala Ala Thr Leu Ser Ile Pro Leu Pro Val Ser Pro Gly
2036      35      40      45
2038 Arg Gly Tyr Ala Pro Thr Gly Ala Leu Asn Tyr His Ser Arg Ser Gly
2039      50      55      60
2041 Asn Gly Pro Phe Gly Ile Gly Trp Gly Ile Gly Gly Ala Ala Val Gln
2042 65      70      75      80
2044 Arg Arg Thr Arg Asn Gly Ala Pro Thr Tyr Asp Asp Thr Asp Glu Phe
2045      85      90      95
2047 Thr Gly Pro Asp Gly Glu Val Leu Val Pro Ala Leu Thr Ala Ala Gly
2048      100      105      110
2050 Thr Gln Glu Ala Arg Gln Ala Thr Ser Leu Leu Gly Ile Asn Pro Gly
2051      115      120      125
2053 Gly Ser Phe Asn Val Gln Val Tyr Arg Ser Arg Thr Glu Gly Ser Leu
2054      130      135      140
2056 Ser Arg Leu Glu Arg Trp Leu Pro Ala Asp Glu Thr Glu Thr Glu Phe
2057 145      150      155      160
2059 Trp Val Leu Tyr Thr Pro Asp Gly Gln Val Ala Leu Leu Gly Arg Asn
2060      165      170      175
2062 Ala Gln Ala Arg Ile Ser Asn Pro Thr Ala Pro Thr Gln Thr Ala Val
2063      180      185      190
2065 Trp Leu Met Glu Ser Ser Val Ser Leu Thr Gly Glu Gln Met Tyr Tyr
2066      195      200      205
2068 Gln Tyr Arg Ala Glu Asp Asp Asp Gly Cys Asp Glu Ala Glu Arg Asp

```

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```

2069      210      215      220
2071 Ala His Pro Gln Ala Gly Ala Gln Arg Tyr Pro Val Ala Val Trp Tyr
2072 225      230      235      240
2074 Gly Asn Arg Gln Ala Ala Arg Thr Leu Pro Ala Leu Val Ser Thr Pro
2075      245      250      255
2077 Ser Met Asp Ser Trp Leu Phe Ile Leu Val Phe Asp Tyr Gly Glu Arg
2078      260      265      270
2080 Ser Ser Val Leu Ser Glu Ala Pro Ala Trp Gln Thr Pro Gly Ser Gly
2081      275      280      285
2083 Glu Trp Leu Cys Arg Gln Asp Cys Phe Ser Gly Tyr Glu Phe Gly Phe
2084      290      295      300
2086 Asn Leu Arg Thr Arg Arg Leu Cys Arg Gln Val Leu Met Phe His Tyr
2087 305      310      315      320
2089 Leu Gly Val Leu Ala Gly Ser Ser Gly Ala Asn Asp Ala Pro Ala Leu
2090      325      330      335
2092 Ile Ser Arg Leu Leu Leu Asp Tyr Arg Glu Ser Pro Ser Leu Ser Leu
2093      340      345      350
2095 Leu Glu Asn Val His Gln Val Ala Tyr Glu Ser Asp Gly Thr Ser Cys
2096      355      360      365
2098 Ala Leu Pro Ala Leu Ala Leu Gly Trp Gln Thr Phe Thr Pro Pro Thr
2099      370      375      380
2101 Leu Ser Ala Trp Gln Thr Arg Asp Asp Met Gly Lys Leu Ser Leu Leu
2102 385      390      395      400
2104 Gln Pro Tyr Gln Leu Val Asp Leu Asn Gly Glu Gly Val Val Gly Ile
2105      405      410      415
2107 Leu Tyr Gln Asp Ser Gly Ala Trp Trp Tyr Arg Glu Pro Val Arg Gln
2108      420      425      430
2110 Ser Gly Asp Asp Pro Asp Ala Val Thr Trp Gly Ala Ala Ala Ala Leu
2111      435      440      445
2113 Pro Thr Met Pro Ala Leu His Asn Ser Gly Ile Leu Ala Asp Leu Asn
2114      450      455      460
2116 Gly Asp Gly Arg Leu Glu Trp Val Val Thr Ala Pro Gly Val Ala Gly
2117 465      470      475      480
2119 Met Tyr Asp Arg Thr Pro Gly Arg Asp Trp Leu His Phe Thr Pro Leu
2120      485      490      495
2122 Ser Ala Leu Pro Val Glu Tyr Ala His Pro Lys Ala Val Leu Ala Asp
2123      500      505      510
2125 Ile Leu Gly Ala Gly Leu Thr Asp Met Val Leu Ile Gly Pro Arg Ser
2126      515      520      525
2128 Val Arg Leu Tyr Ser Gly Lys Asn Asp Gly Trp Asn Lys Gly Glu Thr
2129      530      535      540
2131 Val Gln Gln Thr Glu Arg Leu Thr Leu Pro Val Pro Gly Val Asp Pro
2132 545      550      555      560
2134 Arg Thr Leu Val Ala Phe Ser Asp Met Ala Gly Ser Gly Gln Gln His
2135      565      570      575
2137 Leu Thr Glu Val Arg Ala Asn Gly Val Arg Tyr Trp Pro Asn Leu Gly
2138      580      585      590
2140 His Gly Arg Phe Gly Gln Pro Val Asn Ile Pro Gly Phe Ser Gln Ser
2141      595      600      605

```

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Input Set : A:\1104seq.us1

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```

2143 Val Thr Thr Phe Asn Pro Asp Gln Ile Leu Leu Ala Asp Thr Asp Gly
2144      610      615      620
2146 Ser Gly Thr Thr Asp Leu Ile Tyr Ala Met Ser Asp Arg Leu Val Ile
2147 625      630      635      640
2149 Tyr Phe Asn Gln Ser Gly Asn Tyr Phe Ala Glu Pro His Thr Leu Leu
2150      645      650      655
2152 Leu Pro Lys Gly Val Arg Tyr Asp Arg Thr Cys Ser Leu Gln Val Ala
2153      660      665      670
2155 Asp Ile Gln Gly Leu Gly Val Pro Ser Leu Leu Leu Thr Val Pro His
2156      675      680      685
2158 Val Ala Pro His His Trp Val Cys His Leu Ser Ala Asp Lys Pro Trp
2159      690      695      700
2161 Leu Leu Asn Gly Met Asn Asn Asn Met Gly Ala Arg His Ala Leu His
2162 705      710      715      720
2164 Tyr Arg Ser Ser Val Gln Phe Trp Leu Asp Glu Lys Ala Glu Ala Leu
2165      725      730      735
2167 Ala Ala Gly Ser Ser Pro Ala Cys Tyr Leu Pro Phe Thr Leu His Thr
2168      740      745      750
2170 Leu Trp Arg Ser Val Val Gln Asp Glu Ile Thr Gly Asn Arg Leu Val
2171      755      760      765
2173 Ser Asp Val Leu Tyr Arg His Gly Val Trp Asp Gly Gln Glu Arg Glu
2174      770      775      780
2176 Phe Arg Gly Phe Gly Phe Val Glu Ile Arg Asp Thr Asp Thr Leu Ala
2177 785      790      795      800
2179 Ser Gln Gly Thr Ala Thr Glu Leu Ser Met Pro Ser Val Ser Arg Asn
2180      805      810      815
2182 Trp Tyr Ala Thr Gly Val Pro Ala Val Asp Glu Arg Leu Pro Glu Thr
2183      820      825      830
2185 Tyr Trp Gln Asn Asp Ala Ala Ala Phe Ala Asp Phe Ala Thr Arg Phe
2186      835      840      845
2188 Thr Val Gly Ser Gly Glu Asp Glu Gln Thr Tyr Thr Pro Asp Asp Ser
2189      850      855      860
2191 Lys Thr Phe Trp Leu Gln Arg Ala Leu Lys Gly Ile Leu Leu Arg Ser
2192 865      870      875      880
2194 Glu Leu Tyr Gly Ala Asp Gly Ser Ser Gln Ala Asp Ile Pro Tyr Ser
2195      885      890      895
2197 Val Thr Glu Ser Arg Pro Gln Val Arg Leu Val Glu Ala Asn Gly Asp
2198      900      905      910
2200 Tyr Pro Val Val Trp Pro Met Gly Ala Glu Ser Arg Thr Ser Val Tyr
2201      915      920      925
2203 Glu Arg Tyr His Asn Asp Pro Gln Cys Gln Gln Gln Ala Val Leu Leu
2204      930      935      940
2206 Ser Asp Glu Tyr Gly Phe Pro Leu Arg Gln Val Ser Val Asn Tyr Pro
2207 945      950      955      960
2209 Arg Arg Pro Pro Ser Ala Asp Asn Pro Tyr Pro Ala Ser Leu Pro Ala
2210      965      970      975
2212 Thr Leu Phe Ala Asn Ser Tyr Asp Glu Gln Gln Gln Ile Leu Arg Leu
2213      980      985      990
2215 Gly Leu Gln Gln Ser Ser Ala His His Leu Val Ser Leu Ser Glu Gly

```

Please see explanation on p. 6. Same error.

RAW SEQUENCE LISTING

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Input Set : A:\1104seq.us1

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```

2216          995          1000          1005
2218 His Trp Leu Leu Gly Leu Ala Glu Ala Ser Arg Asp Asp Val Phe Thr
2219          1010          1015          1020
2221 Tyr Ser Ala Asp Asn Val Pro Glu Gly Gly Leu Thr Leu Glu His Leu
E--> 2222 025          1030          1035          1040
2224 Leu Ala Pro Glu Ser Leu Val Ser Asp Ser Gln Val Gly Thr Leu Ala
2225          1045          1050          1055
2227 Gly Gln Gln Gln Val Trp Tyr Leu Asp Ser Gln Asp Val Ala Thr Val
2228          1060          1065          1070
2230 Ala Ala Pro Pro Leu Pro Pro Lys Val Ala Phe Ile Glu Thr Ala Val
2231          1075          1080          1085
2233 Leu Asp Glu Gly Met Val Ser Ser Leu Ala Ala Tyr Ile Val Asp Glu
2234          1090          1095          1100
2236 His Leu Glu Gln Ala Gly Tyr Arg Gln Ser Gly Tyr Leu Phe Pro Arg
E--> 2237 105          1110          1115          1120
2239 Gly Arg Glu Ala Glu Gln Ala Leu Trp Thr Gln Cys Gln Gly Tyr Val
2240          1125          1130          1135
2242 Thr Tyr Ala Gly Ala Glu His Phe Trp Leu Pro Leu Ser Phe Arg Asp
2243          1140          1145          1150
2245 Ser Met Leu Thr Gly Pro Val Thr Val Thr Arg Asp Ala Tyr Asp Cys
2246          1155          1160          1165
2248 Val Ile Thr Gln Trp Gln Asp Ala Ala Gly Ile Val Thr Thr Ala Asp
2249          1170          1175          1180
2251 Tyr Asp Trp Arg Phe Leu Thr Pro Val Arg Val Thr Asp Pro Asn Asp
E--> 2252 185          1190          1195          1200
2254 Asn Leu Gln Ser Val Thr Leu Asp Ala Leu Gly Arg Val Thr Thr Leu
2255          1205          1210          1215
2257 Arg Phe Trp Gly Thr Glu Asn Gly Ile Ala Thr Gly Tyr Ser Asp Ala
2258          1220          1225          1230
2260 Thr Leu Ser Val Pro Asp Gly Ala Ala Ala Leu Ala Leu Thr Ala
2261          1235          1240          1245
2263 Pro Leu Pro Val Ala Gln Cys Leu Val Tyr Val Thr Asp Ser Trp Gly
2264          1250          1255          1260
2266 Asp Asp Asp Asn Glu Lys Met Pro Pro His Val Val Val Leu Ala Thr
E--> 2267 265          1270          1275          1280
2269 Asp Arg Tyr Asp Ser Asp Thr Gly Gln Gln Val Arg Gln Gln Val Thr
2270          1285          1290          1295
2272 Phe Ser Asp Gly Phe Gly Arg Glu Leu Gln Ser Ala Thr Arg Gln Ala
2273          1300          1305          1310
2275 Glu Gly Asn Ala Trp Gln Arg Gly Arg Asp Gly Lys Leu Val Thr Ala
2276          1315          1320          1325
2278 Ser Asp Gly Leu Pro Val Thr Val Ala Thr Asn Phe Arg Trp Ala Val
2279          1330          1335          1340
2281 Thr Gly Arg Ala Glu Tyr Asp Asn Lys Gly Leu Pro Val Arg Val Tyr
E--> 2282 345          1350          1355          1360
2284 Gln Pro Tyr Phe Leu Asp Ser Trp Gln Tyr Val Ser Asp Asp Ser Ala
2285          1365          1370          1375
2287 Arg Gln Asp Leu Tyr Ala Asp Thr His Phe Tyr Asp Pro Thr Ala Arg
2288          1380          1385          1390

```

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Input Set : A:\1104seq.us1

Output Set: N:\CRF3\03212002\J070489.raw

2290 Glu Trp Gln Val Ile Thr Ala Lys Gly Glu Arg Arg Gln Val Leu Tyr
2291 1395 1400 1405
2293 Thr Pro Trp Phe Val Val Ser Glu Asp Glu Asn Asp Thr Val Gly Leu
2294 1410 1415 1420
2296 Asn Asp Ala Ser
E--> 2297 425

VERIFICATION SUMMARY

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Output Set: N:\CRF3\03212002\J070489.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:161 M:254 E: No. of Bases conflict, LENGTH:Input:145 Counted:2344 SEQ:1
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:275 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:311 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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Input Set : A:\1104seq.us1

Output Set: N:\CRF3\03212002\J070489.raw

L:351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:1763 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:2222 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5